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SEQUENCE LISTING

<110> Rory A.J. Curtis

<120> 55053, A Novel Human Eukaryotic Kinase
and Uses Therefor

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His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn	
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Leu Leu Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val	
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 Val His Ala Phe Leu Ser Ile Pro Ser Leu Ser His Ser Val Leu Ser
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Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu Arg	
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595 600 605	
ttc ctc gtg cta aag gac aaa cct ctc agc agc atc aaa gca gac atc	1872
Phe Leu Val Leu Lys Asp Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile	
610 615 620	
gtc cat gcc ttt ctg tcg atc ccc agc ctg agt cac agt gtg ctg tca	1920
Val His Ala Phe Leu Ser Ile Pro Ser Leu Ser His Ser Val Leu Ser	
625 630 635 640	
cag acc agc ttc agg gcc gag tac aag gcc agt ggc ggc ccc tcc gtc	1968
Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala Ser Gly Gly Pro Ser Val	
645 650 655	
ttc caa aag ccc gtc cgc ttc cag gtg gac atc agc tcc tct gag ggt	2016
Phe Gln Lys Pro Val Arg Phe Gln Val Asp Ile Ser Ser Ser Glu Gly	
660 665 670	
cca gag ccc tcc ccg cga cgg gac ggc agc gga ggt ggt ggc atc tac	2064
Pro Glu Pro Ser Pro Arg Arg Asp Gly Ser Gly Gly Gly Ile Tyr	
675 680 685	
tcc gtc acc ttc act ctc atc tcg ggt ccc agc cgt cgg ttc aag cga	2112
Ser Val Thr Phe Thr Leu Ile Ser Gly Pro Ser Arg Arg Phe Lys Arg	
690 695 700	
gtg gtg gag acc atc cag gca cag ctc ctg agc act cat gac cag ccc	2160
Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Gln Pro	
705 710 715 720	
tcc gtg cag gcc ctg gca gac gag aag aac ggg gcc cag acc cgg cct	2208
Ser Val Gln Ala Leu Ala Asp Glu Lys Asn Gly Ala Gln Thr Arg Pro	
725 730 735	

- 10 -

gct ggt gcc cca ccc cga agc ctg cag ccc cca ccc ggc cgc cca gac 2256
Ala Gly Ala Pro Pro Arg Ser Leu Gln Pro Pro Pro Gly Arg Pro Asp
740 745 750

cca gag ctg agc agc tct ccc cgc cga ggc ccc ccc aag gac aag aag 2304
Pro Glu Leu Ser Ser Ser Pro Arg Arg Gly Pro Pro Lys Asp Lys Lys
755 760 765

ctc ctg gcc acc aac ggg acc cct ctg ccc 2334
Leu Leu Ala Thr Asn Gly Thr Pro Leu Pro
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<220>
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<223> Xaa= Leu, Ile, Val, Met, Phe, or Tyr

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<222> 11, 12, 13
<223> Xaa= Leu, Ile, Val, Met, Phe, Tyr, Cys, or Thr

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Xaa Xaa Xaa Xaa Asp Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa
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<210> 5
<211> 278
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<220>
<223> Eukaryotic protein kinase domain

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1 5 10 15
Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
20 25 30

- 11 -

Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
 35 40 45
 His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
 50 55 60
 His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe Asp
 65 70 75 80
 Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
 85 90 95
 Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
 100 105 110
 Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
 115 120 125
 Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
 130 135 140
 Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
 145 150 155 160
 Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
 165 170 175
 Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
 180 185 190
 Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile
 195 200 205
 Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
 210 215 220
 Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
 225 230 235 240
 Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
 245 250 255
 Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
 260 265 270
 Leu Asn His Pro Trp Phe
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<210> 6
 <211> 41
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 <213> Artificial Sequence

<220>
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 Glu Asp Glu Glu Lys Ile Glu Gln Leu Val Glu Met Gly Phe Asp Arg
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 Glu Glu Val Val Lys Ala Leu Arg Ala Thr Asn Gly Asn Gly Val Glu
 20 25 30
 Arg Ala Ala Glu Trp Leu Leu Ser His
 35 40

<210> 7
 <211> 231
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> serkin_6 domain

- 12 -

<400> 7

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Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
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Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
          20          25          30
Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
          35          40          45
Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
          50          55          60
Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65          70          75          80
Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
          85          90          95
Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
          100          105          110
Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
          115          120          125
Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
          130          135          140
Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145          150          155          160
Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
          165          170          175
Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
          180          185          190
Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
          195          200          205
Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
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Ile Lys Ala His Pro Phe Phe
225          230

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<210> 8

<211> 280

<212> PRT

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<220>

<223> tyrkin_6 domain

<400> 8

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Leu Thr Leu Gly Lys Lys Leu Gly Glu Gly Ala Phe Gly Glu Val Tyr
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Lys Gly Thr Leu Lys Ile Glu Val Ala Val Lys Thr Leu Lys Glu Asp
          20          25          30
Ala Lys Glu Glu Phe Leu Arg Glu Ala Lys Ile Met Lys Lys Leu Gly
          35          40          45
Gly Lys His Pro Asn Ile Val Lys Leu Leu Gly Val Cys Thr Glu Glu
          50          55          60
Gly Arg Arg Phe Met Glu Val Glu Pro Leu Met Ile Val Met Glu Tyr
65          70          75          80
Met Glu Gly Gly Asp Leu Leu Asp Tyr Leu Arg Lys Asn Arg Pro Lys
          85          90          95
Leu Ser Leu Ser Asp Leu Leu Ser Phe Ala Leu Gln Ile Ala Lys Gly
          100          105          110
Met Glu Tyr Leu Glu Ser Lys Asn Phe Val His Arg Asp Leu Ala Ala
          115          120          125
Arg Asn Cys Leu Val Gly Glu Asn Lys Val Val Lys Ile Ser Asp Phe
          130          135          140

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Gly 145	Leu	Ser	Arg	Asp	Leu 150	Tyr	Asp	Asp	Asp	Lys 155	Lys	Gly	Glu	Ser	Lys 160
Asp	Tyr	Tyr	Arg	Lys 165	Lys	Gly	Gly	Lys	Gly	Gly	Lys	Thr	Leu	Leu	Pro 175
Ile	Arg	Trp	Met	Ala 180	Pro	Glu	Ser	Leu	Lys	Asp	Gly	Lys	Phe	Thr	Ser
Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Thr
Leu	Gly	Glu	Gln	Pro	Tyr	Pro	Gly	Glu	Ile	Gln	Gln	Phe	Met	Ser	Asn
Glu	Glu	Val	Leu	Glu	Tyr	Leu	Lys	Lys	Gly	Tyr	Arg	Leu	Pro	Lys	Pro
Glu	Asn	Asp	Leu	Pro	Ile	Ser	Ser	Val	Thr	Cys	Pro	Asp	Glu	Leu	Tyr
Asp	Leu	Met	Leu	Gln	Cys	Trp	Ala	Glu	Asp	Pro	Glu	Asp	Arg	Pro	Thr
Phe	Ser	Glu	Leu	Val	Glu	Arg	Leu								